

SEQUENCE LISTING

<110> Kharbanda, Surrender
Kufe, Donald

<120> Modulation of Interaction of MUC1 with MUC1 Ligands

<130> ILEX:094WO

<140> Unknown

<141> 2004-10-21

<150> 60/514,198

<151> 2003-10-24

<150> 60/519,822

<151> 2003-11-12

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 164

<212> PRT

<213> Homo sapiens

<400> 1

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
20 25 30

Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn
50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg
65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu
85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu
100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr
115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
 130 135 140

Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
 145 150 155 160

Ser Gly Ala Gly

<210> 2
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 <212> DNA
 <213> Homo sapiens

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 ggtggagaaa aggagacttc ggctaccag agaagttcag tgcccagctc tactgagaag 180
 aatgcttttta attcctctct ggaagatccc agcaccgact actaccaaga gctgcagaga 240
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 atcaatgtcc acgacatgga gacacagttc aatcagtata aaacggaagc agcctctcga 420
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<210> 3
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 <212> PRT
 <213> Homo sapiens

<400> 3

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
 50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
1          5          10         15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
          20          25          30
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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

 Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
 50 55 60

 Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
 65 70 75 80

 Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
 85 90 95

 Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
 100 105 110

 Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
 115 120 125

 Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
 130 135 140

 Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
 145 150 155 160

 Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 165 170

<210> 6

<211> 519

<212> DNA

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<400> 6

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 cagagaagtt cagtgccag ctctactgag aagaatgctc tgtctactgg ggtctctttc 180
 tttttcctgt cttttcacat ttcaaacctc cagtttaatt cctctctgga agatcccagc 240
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 ttgactctgg ctttccgaga aggtaccatc aatgtccacg acatggagac acagttcaat 420
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<210> 7
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<400> 7

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr
 35 40 45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
 50 55 60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
 65 70 75 80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr
 85 90 95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu
 100 105 110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
 115 120 125

Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 130 135 140

<210> 8
 <211> 420
 <212> DNA
 <213> Homo sapiens

<400> 8

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 cagagaagtt cagtgccag caccgactac taccaagagc tgcagagaga catttctgaa 180
 atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 240
 ccaggatctg tggtggtaca attgactctg gccttcgag aaggtaccat caatgtccac 300
 gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 360

atctcagacg tcagcgtgag tgatgtgccca tttcctttct ctgccagtc tggggctggg 420

<210> 9
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 <212> PRT
 <213> Homo sapiens

<400> 9

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg
 50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu
 65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
 85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
 100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
 115 120 125

Ala Gly
 130

<210> 10
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 10

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gttacagggt ctgggtcatgc aagctctacc ccagggtggag aaaaggagac ttcgggtacc 120

cagagaagtt cagtgccag ctctactgag aagaatgcta tcccagcacc gactactacc 180

aagagctgca gagagacatt tctgaaatgg ccaggatctg tgggtgtaca attgactctg 240

gccttccgag aaggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa 300

acggaagcag cctctcgata taacctgacg atctcagacg tcagcgtgag tgatgtgcca 360
 tttcctttct ctgcccagtc tggggctggg 390

<210> 11
 <211> 102
 <212> PRT
 <213> Homo sapiens
 <400> 11

Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu
 1 5 10 15

Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly
 20 25 30

Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
 35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
 50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
 65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
 85 90 95

Ala Gln Ser Gly Ala Gly
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<210> 12
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 ttcaggccag gatctgtggt ggtacaattg actctggcct tccgagaagg taccatcaat 180
 gtccacgaca tggagacaca gttcaatcag tataaaacgg aagcagcctc tcgatataac 240
 ctgacgatct cagacgtcag cgtgagtgat gtgccatttc ctttctctgc ccagtctggg 300
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<210> 13

<211> 375
 <212> PRT
 <213> Homo sapiens

<400> 13

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1 5 10 15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115 120 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130 135 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145 150 155 160

Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
 165 170 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
 180 185 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
 195 200 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
 210 215 220

Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
225 230 235 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
245 250 255

Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu
260 265 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
275 280 285

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly
290 295 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
340 345 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
355 360 365

Ser Ala Gln Ser Gly Ala Gly
370 375

<210> 14
<211> 1125
<212> DNA
<213> Homo sapiens

<400> 14
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cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
ctctccagcc acagccccgg ttcagggtcc tccaccactc agggacagga tgtcactctg 240
gccccggcca cggaaccagc ttcagggtca gctgccacct ggggacagga tgtcacctcg 300
gtcccagtca ccaggccagc cctggggtcc accaccccg cagcccacga tgtcacctca 360
gccccggaca acaagccagc cccgggtcc accgcccccc cagcccacgg tgtcacctcg 420

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gccccggaca ccaggccggc cccgggctcc accgcccccc cagcccatgg tgtcacctcg      480
gccccggaca acaggcccg cttgggctcc accgcccctc cagtccacaa tgtcacctcg      540
gcctcaggct ctgcatcagg ctgagcttct actctgggtgc acaacggcac ctctgccagg      600
gctaccacaa ccccagccag caagagcact ccattctcaa ttcccagcca ccactctgat      660
actcctacca cccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc      720
acgggtacct ctctcacctc ctccaatcac agcaattctc cccagttgtc tactgggggtc      780
tctttctttt tcctgtcttt tcacatttca aacctccagt ttaattcctc tctggaagat      840
cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt      900
tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg      960
gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag     1020
ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc     1080
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<210> 15
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 15

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
1          5          10          15

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
          20          25          30

```

```

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
          35          40          45

```

```

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
          50          55          60

```

```

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65          70          75          80

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Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
          85          90          95

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Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
          100          105          110

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Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Asn Arg Pro

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115					120					125					
Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala	Ser
130					135					140					
Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr	Ser
145				150						155					160
Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	Ile
			165						170					175	
Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser	Thr
			180					185					190		
Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu	Thr
		195					200					205			
Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser	Phe
	210					215					220				
Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser	Leu
225				230						235					240
Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile	Ser
			245					250						255	
Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu	Ser
			260					265					270		
Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu	Ala
		275					280					285			
Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn
	290					295					300				
Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp
305				310						315					320
Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala
			325					330						335	

Gly

<210> 16
 <211> 1011

<212> DNA

<213> Homo sapiens

<400> 16

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cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta      180
ctctccagcc acagccccgg ttcagggtcc tccaccactc agggacagga tgtcactctg      240
gccccggcca cggaaccagc ttcagggtca gctgccacct ggggacagga tgtcacctcg      300
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gccccggaca acaagaacag gcccgcttg ggctccaccg cccctccagt ccacaatgtc      420
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tctgatactc ctaccacctc tgccagccat agcaccaaga ctgatgccag tagcactcac      600
catagcacgg tacctctctc cacctctctc aatcacagca cttctcccca gttgtctact      660
ggggtctctt tctttttcct gtcttttcac atttcaaacc tccagtttaa ttcctctctg      720
gaagatccca gcaccgacta ctaccaagag ctgcagagag acatttctga aatgtttttg      780
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gtggtggtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacgtggag      900
acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac      960
gtcagcgtga gtgatgtgcc atttcctttc tctgccagtc ctggggctgg g      1011

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<210> 17

<211> 175

<212> PRT

<213> Homo sapiens

<400> 17

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Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
1           5           10           15

His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
20           25           30

Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
35           40           45

Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
50           55           60

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Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
65 70 75 80

Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
85 90 95

Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
100 105 110

Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
115 120 125

Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
130 135 140

Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
145 150 155 160

Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
165 170 175

<210> 18
<211> 525
<212> DNA
<213> Homo sapiens

<400> 18
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acggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactggggtc 180
tctttctttt tctgtcttt tcacatttca aacctccagt ttaattctc tctggaagat 240
cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 300
tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 360
gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 420
ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 480
gtgagtgatg tgccatttcc tttctctgcc cagtctgggg ctggg 525

<210> 19
<211> 58
<212> PRT
<213> Homo sapiens

<400> 19

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
50 55

<210> 20

<211> 174

<212> DNA

<213> Homo sapiens

<400> 20

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gacgtcagcg tgagtgatgt gccatttcct ttctctgccc agtctggggc tggg 174

<210> 21

<211> 50

<212> PRT

<213> Homo sapiens

<400> 21

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro
50

<210> 22

<211> 150

<212> DNA

<213> Homo sapiens

<400> 22

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gacgtcagcg tgagtgatgt gccatttcct

150

<210> 23

<211> 49

<212> PRT

<213> Homo sapiens

<400> 23

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
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Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
 20 25 30

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
 35 40 45

Gly

<210> 24

<211> 147

<212> DNA

<213> Homo sapiens

<400> 24

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cctttctctg cccagtctgg ggctggg 147

<210> 25

<211> 120

<212> PRT

<213> Homo sapiens

<400> 25

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
 1 5 10 15

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
100 105 110

Phe Ser Ala Gln Ser Gly Ala Gly
115 120

<210> 26
<211> 360
<212> DNA
<213> Homo sapiens

<400> 26
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atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 180
ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
atctcagacg tcagcgtgag tgatgtgcca tttcctttct ctgccagtc tggggctggg 360

<210> 27
<211> 77
<212> PRT
<213> Homo sapiens

<400> 27

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly

65

70

75

<210> 28
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 28
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 gtggtggtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacatggag 120
 acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180
 gtcagcgtga gtgatgtgcc atttcctttc tctgcccagt ctggggctgg g 231

<210> 29
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 29

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
 1 5 10 15

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
 65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
 85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
 100 105 110

<210> 30
 <211> 336
 <212> DNA
 <213> Homo sapiens

<400> 30
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 atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 180
 ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
 gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
 atctcagacg tcagcgtgag tgatgtgcca tttcct 336

<210> 31
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 31

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
 1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
 20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
 35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
 50 55 60

Asp Val
 65

<210> 32
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 32
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 acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180
 gtcagcgtga gtgatgtg 198

<210> 33
 <211> 232
 <212> PRT
 <213> HS

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15												
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25					30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			100					105					110		
Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
145					150					155					160
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Val	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										
<210>	34														
<211>	699														

<212> DNA

<213> HS

<400> 34

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gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg      60
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccg      120
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg      420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      540
cccgtgctgg actccgtcgg ctcttcttct ctctacagca agctcacctg ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
tacacgcaga agagcctctc cctgtctccg ggtaaata      699

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<210> 35

<211> 230

<212> PRT

<213> HS

<400> 35

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Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu
1          5          10          15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20          25          30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35          40          45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
50          55          60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65          70          75          80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
85          90          95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

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100	105	110
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu		
115	120	125
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		
130	135	140
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
145	150	155
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala		
165	170	175
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
180	185	190
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
195	200	205
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
210	215	220
Ser Leu Ser Pro Gly Lys		
225	230	

<210> 36
 <211> 690
 <212> DNA
 <213> HS

<400> 36
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 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 120
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240
 agcacgtacc gtgtgggtcag cgtcctcacc gtctgcacc aggactgggt gaatggcaag 300
 gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 360
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 420
 ctgaccaaga accaggtcag cctgacctgc ctagtcaaag gcttctatcc cagcgacatc 480
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaaggccac gcctcccgtg 540
 ctggactccg acggtctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660

cagaagagcc tctccctgtc tccgggtaaa 690

<210> 37

<211> 228

<212> PRT

<213> HS

<400> 37

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

195

200

205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220

Ser Pro Gly Lys
 225

<210> 38
 <211> 687
 <212> DNA
 <213> HS

<400> 38
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 acgtgctgtg tggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 180
 gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 240
 ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 300
 aagtgaagg tctccaacaa aggcctccca gccccatcg agaaaacat ctccaaaacc 360
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 420
 aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct accccagcga catcgccgtg 480
 gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 540
 tccgacggct ccttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
 gggaaacgtt tctcatgctc cgtgatgcat gaggtctctg acaaccacta cacacagaag 660
 agcctctccc tgtctccggg taaatga 687

<210> 39
 <211> 229
 <212> PRT
 <213> Homo Sapiens

<400> 39

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
 50 55 60
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110
 Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125
 Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 180 185 190
 Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 195 200 205
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 210 215 220
 Leu Ser Leu Gly Lys
 225

<210> 40
 <211> 690
 <212> DNA
 <213> HS

<400> 40
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 tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gaccctgag 120
 gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 180
 gtggatggcg tggaggtgca taatgccaaag acaaagccgc gggaggagca gttcaacagc 240


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acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgar cggcaaggag      300
tacaagtgca aggtctccar caaaggcctc ccgtcctcca tcgagaaaac catctccaam      360
gccamagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg      420
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc      480
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgctgctg      540
gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag cagktggcag      600
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag      660
aagagcctct ccctgtctct gggtaaata      690

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<210> 41
<211> 585
<212> PRT
<213> HS

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<400> 41

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Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1          5          10          15

```

```

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
          20          25          30

```

```

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
          35          40          45

```

```

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
          50          55          60

```

```

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65          70          75          80

```

```

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
          85          90          95

```

```

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
          100          105          110

```

```

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
          115          120          125

```

```

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
          130          135          140

```

Arg His Pro Tyr Phe Tyr Ala Pro Gln Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Pro Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Met Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

<210>	42
<211>	1758
<212>	DNA
<213>	HS

27/36

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aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt 240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa 300
tgcttcttgc aacacaaaga tgacaatcca aatctccccc gattggtgag accagagggtt 360
gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat 420
gaaattgcca gaagacatcc ttacttttat gccccgcaac tccttttctt tgctaaaagg 480
tataaagctg cttttacaga atgttgccaa gctgctgata aagcagcctg cctgttgcca 540
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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc 660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa 720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt 780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa 840
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atggaagagc ctcaagaattt aatcaaacaa aattgtgagc tttttgagca gcttgagag 1200
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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggctct gaaccagtta 1380
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aaagagcaac tgaaagctgt tatggatgat ttgcgagctt ttgtagagaa gtgctgcaag 1680
gctgacgata aggaaacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa 1740
gctgccttag gcttataa 1758

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<210> 43
<211> 110
<212> PRT
<213> Homo Sapiens

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<400> 43

Met Arg Phe Met Thr Leu Leu Phe Leu Thr Ala Leu Ala Gly Ala Leu
 1 5 10 15

Val Cys Ala Tyr Asp Pro Glu Ala Ala Ser Ala Pro Gly Ser Gly Asn
 20 25 30

Pro Cys His Glu Ala Ser Ala Ala Gln Lys Glu Asn Ala Gly Glu Asp
 35 40 45

Pro Gly Leu Ala Arg Gln Ala Pro Lys Pro Arg Lys Gln Arg Ser Ser
 50 55 60

Leu Leu Glu Lys Gly Leu Asp Gly Ala Lys Lys Ala Val Gly Gly Leu
 65 70 75 80

Gly Lys Leu Gly Lys Asp Ala Val Glu Asp Leu Glu Ser Val Gly Lys
 85 90 95

Gly Ala Val His Asp Val Lys Asp Val Leu Asp Ser Val Leu
 100 105 110

<210> 44

<211> 333

<212> DNA

<213> HS

<400> 44

atgagggttca tgactctcct cttcctgaca gctctggcag gagccctggg ctgtgcctat 60
 gatccagagg ccgcctctgc cccaggatcg ggggaaccctt gccatgaagc atcagcagct 120
 caaaaggaaa atgcaggtga agaccagggt ttagccagac aggcaccaa gccaaaggaag 180
 cagagatcca gccttctgga aaaaggccta gacggagcaa aaaaagctgt ggggggactc 240
 ggaaaactag gaaaagatgc agtcgaagat ctagaaagcg tgggtaaagg agccgtccat 300
 gacgttaaag acgtccttga ctcagtacta tag 333

<210> 45

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Synthesized Sequence

<400> 45

aacccttgcc atgaagcatc a

21

<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 46
aagcatcagc agctcaaaag g 21

<210> 47
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 47
aaaaggaaaa tgcaggtgaa g 21

<210> 48
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 48
aaaggaaaat gcaggtgaag a 21

<210> 49
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 49
aaggaaaatg caggtgaaga c 21

<210> 50
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Sythesized Sequence

<400> 50
aaaatgcagg tgaagaccca g 21

<210> 51
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized sequence

<400> 51
aaatgcaggt gaagacccag g 21

<210> 52
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 52
aaagccaagg aagcagagat c 21

<210> 53
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 53
aagccaagga agcagagatc c 21

<210> 54
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 54
aaggaagcag agatccagcc t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 55
aagcagagat ccagccttct g 21

<210> 56

<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 56
aaaaaggcct agacggagca a 21

<210> 57
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized sequence

<400> 57
aaaaggccta gacggagcaa a 21

<210> 58
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 58
aaaggcctag acggagcaaa a 21

<210> 59
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 59
aaggcctaga cggagcaaaa a 21

<210> 60
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 60
aaactaggaa aagatgcagt c 21

<210> 61
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